

# Package ‘BeadArrayUseCases’

January 14, 2021

**Version** 1.28.0

**Date** 2019-05-29

**Title** Analysing Illumina BeadArray expression data using Bioconductor

**Author** Mark Dunning, Wei Shi, Andy Lynch, Mike Smith, Matt Ritchie

**Description** Example data files and use cases for processing Illumina BeadArray expression data using Bioconductor

**Imports** beadarray (>= 2.3.18), limma, GEOquery

**Suggests** Biostrings, GenomicRanges, illuminaHumanv1.db, illuminaHumanv2.db, illuminaHumanv3.db

**Maintainer** Mike Smith <grimbough@gmail.com>

**License** GPL-2

**biocViews** MicroarrayData

**git\_url** <https://git.bioconductor.org/packages/BeadArrayUseCases>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** 5e935c0

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-01-14

**R topics documented:**